

- 1 -

piece 1, NC_000913, ansPyncG-, config: linear, direction: -, begin: 1524300, end: 1523985

The figure displays a genomic sequence from position 1524300 to 15242200. The top line shows the DNA sequence with RNA genes highlighted in green and blue. The bottom line shows the corresponding mRNA sequence with amino acid translations. Red dots indicate start sites (AUG) and stop sites (UAA, UAG, UGA). The legend indicates: green RNA genes, blue RNA genes, red dot (start), black dot (stop), dash (no gene), and blue text (amino acid translation).

p35 6.2 bits

The figure shows a secondary structure of a ribozyme precursor. The structure is composed of several hairpins and a central domain. Key features include:

- Top Labels:** *1524130, *1524120, *1524110, *1524100, *1524090, *1524080, *1524070, and *1524060.
- Bottom Labels:** fMet, val, ile, thr, ile, ile, ala, arg, met, asn, lys.
- Color Coding:**
 - Red:** A large red box covers the bottom right portion of the structure, containing labels like "ir ansP_yncG-".
 - Green:** A green box is located at the bottom left, containing labels "p10" and "4.6 bits".
 - Yellow:** Yellow boxes are scattered throughout the structure, often associated with specific nucleotides or domains.
- Annotations:** Red dots are placed on specific nucleotides, and blue arrows indicate cleavage sites or specific interactions.

... ----- } p35-(23)-p10 1524128 Gap 1.4 bit
----- | p35-p10 1524128 total 9.4 bits

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... -----| p35-p10 1524128 total 9.4 bits
          {-----} sd-(5)-ir 1524090 Gap 5.4 bits
          |-----| sd-ir 1524090 ansP_vncG- total 8.3 bits
          |-----| ir ansP_vncG-
          {-----} sd-(8)-ir 1524087 Gap 2.4 bits
          |-----| sd-ir 1524087 ansP_vncG- total 8.9 bits
          |-----| ... sd-ir 1524049 ansP_vncG-
```

This figure displays a sequence alignment for the sd-(18)-ir 1524049 gene. The top row shows the nucleotide sequence with positions 1524050, 1524040, 1524030, 1524020, 1524010, 1524000, and 1523990 indicated by asterisks. The bottom row shows the corresponding amino acid sequence. A red circle highlights a difference at position 1524010 where the nucleotide is 't' instead of 'a'. The alignment includes a green shaded region representing a match and a yellow shaded region representing a mismatch. Below the sequence, a legend indicates the following color coding: blue for fMet, black for phe, red for met, orange for ala, purple for thr, brown for tyr, pink for met, grey for ser, light blue for leu, light green for lys, dark green for cys, light orange for arg, light pink for ala, light blue for met, light green for ser, light orange for his, light pink for lys, light blue for asp, and light green for thr.

For more information about the study, please contact Dr. John Smith at (555) 123-4567 or via email at john.smith@researchinstitute.org.

A diagram illustrating a sequence of operations or transitions. It features a dashed line at the top, followed by a series of colored arrows pointing to the right. The arrows are colored in various shades of blue, green, orange, and red. To the right of the arrows is a vertical bar, and further to the right are more arrows, continuing the sequence.

「#>#> orf_19_codons

{-----} sd-(9)-ir 1524037 Gap 2.3 bits
{-----} sd-ir 1524037 ansP vncG- total 7.1 bits